

RAW SEQUENCE LISTING

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Application Serial Number: 10/530,240
Source: Pat 10
Date Processed by STIC: 9/19/05

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RAW SEQUENCE LISTING

DATE: 09/19/2005

PATENT APPLICATION: US/10/530,240

TIME: 14:14:35

Input Set : A:\BB-142.ST25.txt

Output Set: N:\CRF4\09192005\J530240.raw

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3 <110> APPLICANT: Muller, Werner
4     Schroeder, Heinz
5     Krasko, Anatoli
7 <120> TITLE OF INVENTION: Decomposition and Modification of Silicate and Silicone by
8     Silicase and Use of the Reversible Enzyme
10 <130> FILE REFERENCE: BB-142
12 <140> CURRENT APPLICATION NUMBER: 10/530,240
13 <141> CURRENT FILING DATE: 2005-04-04
15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010983
16 <151> PRIOR FILING DATE: 2003-10-02
18 <150> PRIOR APPLICATION NUMBER: DE 10246186.4
19 <151> PRIOR FILING DATE: 2002-10-03
21 <160> NUMBER OF SEQ ID NOS: 2
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1396
27 <212> TYPE: DNA
28 <213> ORGANISM: Suberites domuncula
30 <400> SEQUENCE: 1
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33 tagtactagt agtctacaag aacaactgtc aacaactgtc agattatgtg tataaaccaa      120
35 gatgtctgca attcttaaga gaaacgtacc tatccaaaga gtcggtctcc cactgacctc      180
37 ctatgtcagt agatgggctt ctgctctgcc caccaggacc catccttttt acaagttggt      240
39 tgatgacagt accaccccag tgacaaggtc tactcttctc agtgctcata tggttgacac      300
41 cttgctagat gagaaccagc agagcagaca tgaaaaccaa cacacagaca cgtcttacia      360
43 aatgtaccag ggattaaaat ttgttgtaaa gacgctgttt actccatcga aatgccaccg      420
45 tcacttctcc acatcagctc atttgtctgc catgggtcga catcaatccc ccatcaatat      480
47 aatcacctcc agtacgacca aaggaccgctc attgaaaccg ttaaaattta gcaagagttg      540
49 ggacaagcca gtaatcggca ccgtcaaaga tactggctat tatcttaaat ttgcaccaga      600
51 atctgcagca gagaagtgca cattgcatac gtacaatggt gaatatatcc tagatcattt      660
53 ccattatcac tgggggaaga aggatgggga aggagcagag catttcatcg atggaaaaca      720
55 atacgacatc gagttccact ttgtacataa aaagggtggg ttgactgac cagatgctag      780
57 agacgctttt gctgttttgg gcgtttttgg aaaggccgac cctcgtttga agatcaatgg      840
59 aatctgggag ctactctcac cgtcaactgt cctgactgtc gactcaacac gaaacgtcgc      900
61 tgatgttggt ccctctaagc ttctcccaag tgccagagac tatttttact atgaaggttc      960
63 ttgaccaca cctacgtatg gtgaggttgt gcactgggtt gttctcaatg aacctatagc     1020
65 tgcacctagt gagtatctgt cagctctgag acagatgcaa gctgacaaag aaggtactgt     1080
67 gattgactca aactatcgag agcttcaaga agtccacaat cgacctgtgc aacgatttaa     1140
69 gagtgatgag caagggagag gagaatttga cgatatttct aagaatgagg acattgtgga     1200
71 ggacttgtct aaattgtctg gtaactttat tagagagctg gtcaggaaga tatattggtg     1260
73 acctttttct acacttgtaa gagttttagg ccagaataca ttcatcatt tggactgtta     1320
75 ttttgtgtac actgcttagc agtttatata aacactacaa tgccattatt ataatatagc     1380
77 caatgctgtg atttga                                     1396

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80 <210> SEQ ID NO: 2
81 <211> LENGTH: 379
82 <212> TYPE: PRT
83 <213> ORGANISM: Suberites domuncula
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91 Pro Leu Thr Ser Tyr Val Ser Arg Trp Ala Ser Ala Leu Pro Thr Arg
92 20 25 30
95 Thr His Pro Phe Tyr Lys Leu Val Asp Asp Ser Thr Thr Pro Val Thr
96 35 40 45
99 Arg Ser Thr Leu Leu Ser Ala His Met Val Asp Thr Leu Leu Asp Glu
100 50 55 60
103 Asn Gln Gln Ser Arg His Glu Asn Gln His Thr Asp Thr Ser Tyr Lys
104 65 70 75 80
107 Met Tyr Gln Gly Leu Lys Phe Val Val Lys Thr Leu Phe Thr Pro Ser
108 85 90 95
111 Lys Cys His Arg His Phe Ser Thr Ser Ala His Leu Ser Ala Met Gly
112 100 105 110
115 Arg His Gln Ser Pro Ile Asn Ile Ile Thr Ser Ser Thr Thr Lys Gly
116 115 120 125
119 Pro Ser Leu Lys Pro Leu Lys Phe Ser Lys Ser Trp Asp Lys Pro Val
120 130 135 140
123 Ile Gly Thr Val Lys Asp Thr Gly Tyr Tyr Leu Lys Phe Ala Pro Glu
124 145 150 155 160
127 Ser Ala Ala Glu Lys Cys Thr Leu His Thr Tyr Asn Gly Glu Tyr Ile
128 165 170 175
131 Leu Asp His Phe His Tyr His Trp Gly Lys Lys Asp Gly Glu Gly Ala
132 180 185 190
135 Glu His Phe Ile Asp Gly Lys Gln Tyr Asp Ile Glu Phe His Phe Val
136 195 200 205
139 His Lys Lys Val Gly Leu Thr Asp Pro Asp Ala Arg Asp Ala Phe Ala
140 210 215 220
143 Val Leu Gly Val Phe Gly Lys Ala Asp Pro Arg Leu Lys Ile Asn Gly
144 225 230 235 240
147 Ile Trp Glu Leu Leu Ser Pro Ser Thr Val Leu Thr Val Asp Ser Thr
148 245 250 255
151 Arg Asn Val Ala Asp Val Val Pro Ser Lys Leu Leu Pro Ser Ala Arg
152 260 265 270
155 Asp Tyr Phe His Tyr Glu Gly Ser Leu Thr Thr Pro Thr Tyr Gly Glu
156 275 280 285
159 Val Val His Trp Phe Val Leu Asn Glu Pro Ile Ala Val Pro Ser Glu
160 290 295 300
163 Tyr Leu Ser Ala Leu Arg Gln Met Gln Ala Asp Lys Glu Gly Thr Val
164 305 310 315 320
167 Ile Asp Ser Asn Tyr Arg Glu Leu Gln Glu Val His Asn Arg Pro Val
168 325 330 335
171 Gln Arg Phe Lys Ser Asp Glu Gln Gly Arg Gly Glu Phe Asp Asp Ile
172 340 345 350

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175 Ser Lys Asn Glu Asp Ile Val Glu Asp Leu Ser Lys Leu Ser Gly Asn
176 355 360 365
179 Phe Ile Arg Glu Leu Val Arg Lys Ile Tyr Trp
180 370 375

VERIFICATION SUMMARY

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